

attcggtctg agttcacctg gtgtgtgttt gacttcaggc ttttccttct gccagctcc	60
gtcccaccca gcagcccga gagnaaggag gcagctggca ccacactggg ctttggagac	120
actgcgggga ctgtggaccc caccctgtg caccgagctc ctgcaaaagc aaacctgaga	180
accttgggtc ctcccagcgc ccagcc atg ggg gaa ctg tgc tgc agc agc gac tcc	233
Met Gly Glu Leu Cys Arg Arg Asp Ser	
1 5	
gca ctc acg gca ctg gac gag gag aca ctg tgg gag atg atg gag agc	281
Ala Leu Thr Ala Leu Asp Glu Glu Thr Leu Trp Glu Met Met Glu Ser	
10 15 20 25	
cac cgc cac agg atc gta cgc tgc atc tgc ccc agc cgc ctc acc ccc	329
His Arg His Arg Ile Val Arg Cys Ile Cys Pro Ser Arg Leu Thr Pro	
30 35 40	
tac ctg cgc cag gcc aag gtg ctg tgc cag ctg gac gag gag gag gtg	377
Tyr Leu Arg Gln Ala Lys Val Leu Cys Gln Leu Asp Glu Glu Glu Val	
45 50 55	
ctg cac agc ccc cgg ctc acc aac agc gcc atg cgg gcc ggg cac ttg	425
Leu His Ser Pro Arg Leu Thr Asn Ser Ala Met Arg Ala Gly His Leu	
60 65 70	
ctg gat ttg ctg aag act cga ggg aag aac ggg gcc atc gcc ttc ctg	473
Leu Asp Leu Leu Lys Thr Arg Gly Lys Asn Gly Ala Ile Ala Phe Leu	
75 80 85	
gag agc ctg aag ttc cac aac cct gac gtc tac acc ctg gtc acc ggg	521
Glu Ser Leu Lys Phe His Asn Pro Asp Val Tyr Thr Leu Val Thr Gly	
90 95 100 105	
ctg cag cct gat gtt gac ttc agt aac ttt agc ggt ctc atg gag aca	569
Leu Gln Pro Asp Val Asp Phe Ser Asn Phe Ser Gly Leu Met Glu Thr	
110 115 120	
tcc aag ctg acc gag tgc ctg gct ggg gcc atc ggc agc ctg cag gag	617
Ser Lys Leu Thr Glu Cys Leu Ala Gly Ala Ile Gly Ser Leu Gln Glu	
125 130 135	
gag ctg aac cag gaa aag ggg cag aag gag gtg ctg ctg cgg cgg tgc	665
Glu Leu Asn Gln Glu Lys Gly Gln Lys Glu Val Leu Leu Arg Arg Cys	
140 145 150	
cag cag ctg cag gag cac ctg ggc ctg gcc gag acc cgt gcc gag ggc	713
Gln Gln Leu Gln Glu His Leu Gly Leu Ala Glu Thr Arg Ala Glu Gly	
155 160 165	
ctg cac cag ctg gag gct gac cac agc cgc atg aag cgt gag gtt agc	761
Leu His Gln Leu Glu Ala Asp His Ser Arg Met Lys Arg Glu Val Ser	
170 175 180 185	
gca cac ttc cat gag gtg ctg agg ctg aag gac gag atg ctc agc ctc	809
Ala His Phe His Glu Val Leu Arg Leu Lys Asp Glu Met Leu Ser Leu	
190 195 200	

Fig. 1A



cgg gag aag cag cgg ctg gtg cgg atg cat gcc atc tgc ccc aga gac	1529
Arg Glu Lys Gln Arg Leu Val Arg Met His Ala Ile Cys Pro Arg Asp	
430 435 440	
gac agc gac tgc agc ctc gtc agc tcc aca gag tct cag ctc ttg tcg	1577
Asp Ser Asp Cys Ser Leu Val Ser Ser Thr Glu Ser Gln Leu Leu Ser	
445 450 455	
gac ctg agt gcc acg tcc agc cgc gag ctg gtg gac agc ttc cgc tcc	1625
Asp Leu Ser Ala Thr Ser Ser Arg Glu Leu Val Asp Ser Phe Arg Ser	
460 465 470	
agc agc ccc gcg ccc ccc agc cag cag tcc ctg tac aag cgg gtg gcc	1673
Ser Ser Pro Ala Pro Pro Ser Gln Gln Ser Leu Tyr Lys Arg Val Ala	
475 480 485	
gag gac ttc ggg gaa gaa ccc tgg tct ttc agc agc tgc ctg gag atc	1721
Glu Asp Phe Gly Glu Glu Pro Trp Ser Phe Ser Ser Cys Leu Glu Ile	
490 495 500 505	
ccg gag gga gac ccg gga gcc ctg ccg gga gct aag gca ggc gac cca	1769
Pro Glu Gly Asp Pro Gly Ala Leu Pro Gly Ala Lys Ala Gly Asp Pro	
510 515 520	
cac ctg gat tat gag ctc cta gac acg gca gac ctt ccg cag ctg gaa	1817
His Leu Asp Tyr Glu Leu Leu Asp Thr Ala Asp Leu Pro Gln Leu Glu	
525 530 535	
agc agc ctg cag cca gtc tcc cct gga agg ctt gat gtc tcg gag agc	1865
Ser Ser Leu Gln Pro Val Ser Pro Gly Arg Leu Asp Val Ser Glu Ser	
540 545 550	
ggc gtc ctc atg cgg cgg agg cca gcc cgc agg atc ctg agc cag gtc	1913
Gly Val Leu Met Arg Arg Arg Pro Ala Arg Arg Ile Leu Ser Gln Val	
555 560 565	
acc atg ctg gcg ttc cag ggg gat gca ttg ctg gag cag atc agc gtc	1961
Thr Met Leu Ala Phe Gln Gly Asp Ala Leu Leu Glu Gln Ile Ser Val	
570 575 580 585	
atc ggc ggg aac ctc acg ggc atc ttc atc cac cgg gtc acc ccg ggc	2009
Ile Gly Gly Asn Leu Thr Gly Ile Phe Ile His Arg Val Thr Pro Gly	
590 595 600	
tcg gcg gcg gac cag atg gcc ttg cgc ccg ggc acc cag att gtg atg	2057
Ser Ala Ala Asp Gln Met Ala Leu Arg Pro Gly Thr Gln Ile Val Met	
605 610 615	
gtt gat tac gaa gcc tca gag ccc ttg ttc aag gca gtc ctg gag gac	2105
Val Asp Tyr Glu Ala Ser Glu Pro Leu Phe Lys Ala Val Leu Glu Asp	
620 625 630	
acg acc ctg gag gag gcc gtg ggg ctt ctc agg agg gtg gac ggc ttc	2153
Thr Thr Leu Glu Glu Ala Val Gly Leu Leu Arg Arg Val Asp Gly Phe	
635 640 645	

Fig. 1C



atc cag gag gga gag gtg tcc ggg ggc cgc tgc tgg gtg acc cgc cat	2873
Ile Gln Glu Gly Glu Val Ser Gly Gly Arg Cys Trp Val Thr Arg His	
875 880 885	
gct gtg gag tcc ctc atg gaa aag aac acc cat gcc ctc ctg gac gtc	2921
Ala Val Glu Ser Leu Met Glu Lys Asn Thr His Ala Leu Leu Asp Val	
890 895 900 905	
cag ctg gac agt gtc tgc acc ctg cac agg atg gac atc ttc ccc atc	2969
Gln Leu Asp Ser Val Cys Thr Leu His Arg Met Asp Ile Phe Pro Ile	
910 915 920	
gtc atc cac gtc tct gtc aac gag aag atg gca aag aag ctc aag aag	3017
Val Ile His Val Ser Val Asn Glu Lys Met Ala Lys Lys Leu Lys Lys	
925 930 935	
ggc cta cag cgg ttg ggc acc tca gag gag cag ctc ctg gag gct gcg	3065
Gly Leu Gln Arg Leu Gly Thr Ser Glu Glu Gln Leu Leu Glu Ala Ala	
940 945 950	
agg cag gag gag gga gac ctg gac cgg gcg ccc tgt cta tac agc agc	3113
Arg Gln Glu Glu Gly Asp Leu Asp Arg Ala Pro Cys Leu Tyr Ser Ser	
955 960 965	
ctg gct cct gac ggc tgg agc gac ctg gac ggc ctg ctc agc tgt gtc	3161
Leu Ala Pro Asp Gly Trp Ser Asp Leu Asp Gly Leu Leu Ser Cys Val	
970 975 980 985	
cgc cag gcc atc gcc gac gag cag aag aag gtg gtg tgg acg gag cag	3209
Arg Gln Ala Ile Ala Asp Glu Gln Lys Lys Val Val Trp Thr Glu Gln	
990 995 1000	
agc ccc cga tga tgcaccgtgc cccttcccgg gactgtgggg gcttctgtgt	3261
Ser Pro Arg *	
gcctgttaat gcagtccctgt tcctcagccc aggccctctt ggcacagctg tgggctcctt	3321
ggcacatgag gccggctctc ccactgggt ggggtctaac cttgaaccct caccacgtgc	3381
aggtcacaca cagtgaagcc acttgtaact gcacactttt ctgtggaaac atcttcaccc	3441
tttaccaggc ttggcatggt ctgaactgga aaccctgaga atgtttctgc agtaggacag	3501
gagggacatc ttcccatgcc ttccctagaa ccggaggccc cggacttctc tggaaaaccg	3561
cctgtctgca ggccccgattc aaatctatgg gggctgcact tccctttttac attttgatgt	3621
gtcaaaggct tttggagtga ccaaaagcac agaggcagcg ggtggggcgc ctgggtgggtc	3681
cccaaggctg ctgccaccct tgcccggggc agaggcataa gccacatat gctgtgacgc	3741
tggccacctt ttctcagctt ctgaggctgc gatgcctcag gaactccagt ttacagagac	3801
cagtgtgttt acttgtaaat aaagcctctg ggtggtggag acggtacttt cagtgggtct	3861
gtgccccgtg gccccgtgtgc ctgttcggtg ggggtgtccc agagaagcct ggcaccagta	3921
ccccgtcaa	3931

Fig. 1E





V	E	S	L	M	E	K	N	T	H	A	L	L	D	V	Q	L	D	S	V	960
GTG	GAG	TCC	CTC	ATG	GAA	AAG	AAC	ACC	CAT	GCC	CTC	CTG	GAC	GTC	CAG	CTG	GAC	AGT	GTC	2880
C	T	L	H	R	M	D	I	F	P	I	V	I	H	V	S	V	N	E	K	980
TGC	ACC	CTG	CAC	AGG	ATG	GAC	ATC	TTC	CCC	ATC	GTC	ATC	CAC	GTC	TCT	GTC	AAC	GAG	AAG	2940
M	A	K	K	L	K	K	G	L	Q	R	L	G	T	S	E	E	Q	L	L	1000
ATG	GCA	AAG	AAG	CTC	AAG	AAG	GGC	CTA	CAG	CGG	TTG	GGC	ACC	TCA	GAG	GAG	CAG	CTC	CTG	3000
E	A	A	R	Q	E	E	G	D	L	D	R	A	P	C	L	Y	S	S	L	1020
GAG	GCT	GCG	AGG	CAG	GAG	GAG	GGA	GAC	CTG	GAC	CGG	GCG	CCC	TGT	CTA	TAC	AGC	AGC	CTG	3060
A	P	D	G	W	S	D	L	D	G	L	L	S	C	V	R	Q	A	I	A	1040
GCT	CCT	GAC	GGC	TGG	AGC	GAC	CTG	GAC	GGC	CTG	CTC	AGC	TGT	GTC	CGC	CAG	GCC	ATC	GCC	3120
D	E	Q	K	K	V	Q	R	R	R	H	P	R	I	N	P	S	Q	R	T	1060
GAC	GAG	CAG	AAG	AAG	GTG	CAA	CGC	CGA	CGT	CAT	CCA	AGA	ATT	AAC	CCA	AGC	CAG	AGG	ACG	3180
G	I	A	T	Q	Q	R	Q	C	H	R	R	I	N	P	R	Q	R	M	G	1080
GGC	ATC	GCC	ACC	CAG	CAA	CGC	CAG	TGT	CAC	CGA	AGA	ATT	AAC	CCA	AGG	CAG	AGG	ATG	GGC	3240
I	A	T	Q	Q	R	Q	C	H	R	R	I	N	P	S	Q	R	T	G	I	1100
ATT	GCC	ACC	CAG	CAA	CGC	CAG	TGT	CAC	CGA	AGA	ATT	AAC	CCA	AGC	CAG	AGG	ACG	GGC	ATC	3300
T	T	Q	Q	C	Q	C	H	R	R	I	N	P	S	Q	R	T	G	I	A	1120
ACC	ACC	CAG	CAA	TGC	CAG	TGT	CAC	CGA	AGA	ATT	AAC	CCA	AGC	CAG	AGG	ACG	GGC	ATC	GCC	3360
M	P	S	S	S	D	T	L	K	K	D	K	L	L	P	R	N	T	T		1139
ATG	CCT	TCA	TCT	TCG	GAC	ACT	CTC	AAA	AAA	GAT	AAG	CTT	CTG	CCC	AGA	AAC	ACC	ACA		3417

Fig. 2C



1.4M

CRD

DNA\_pol\_1000bp

CRDnew

RSBds\_new

SH3\_2

SH3\_Guanylate\_in

1 41 81 121 161 201 241 281 321 361 401 441 481 521 561 601 641 681 721 761 801 841 881 921 961 1001 1041 1081 1121

Can  
Mod

Fig. 3

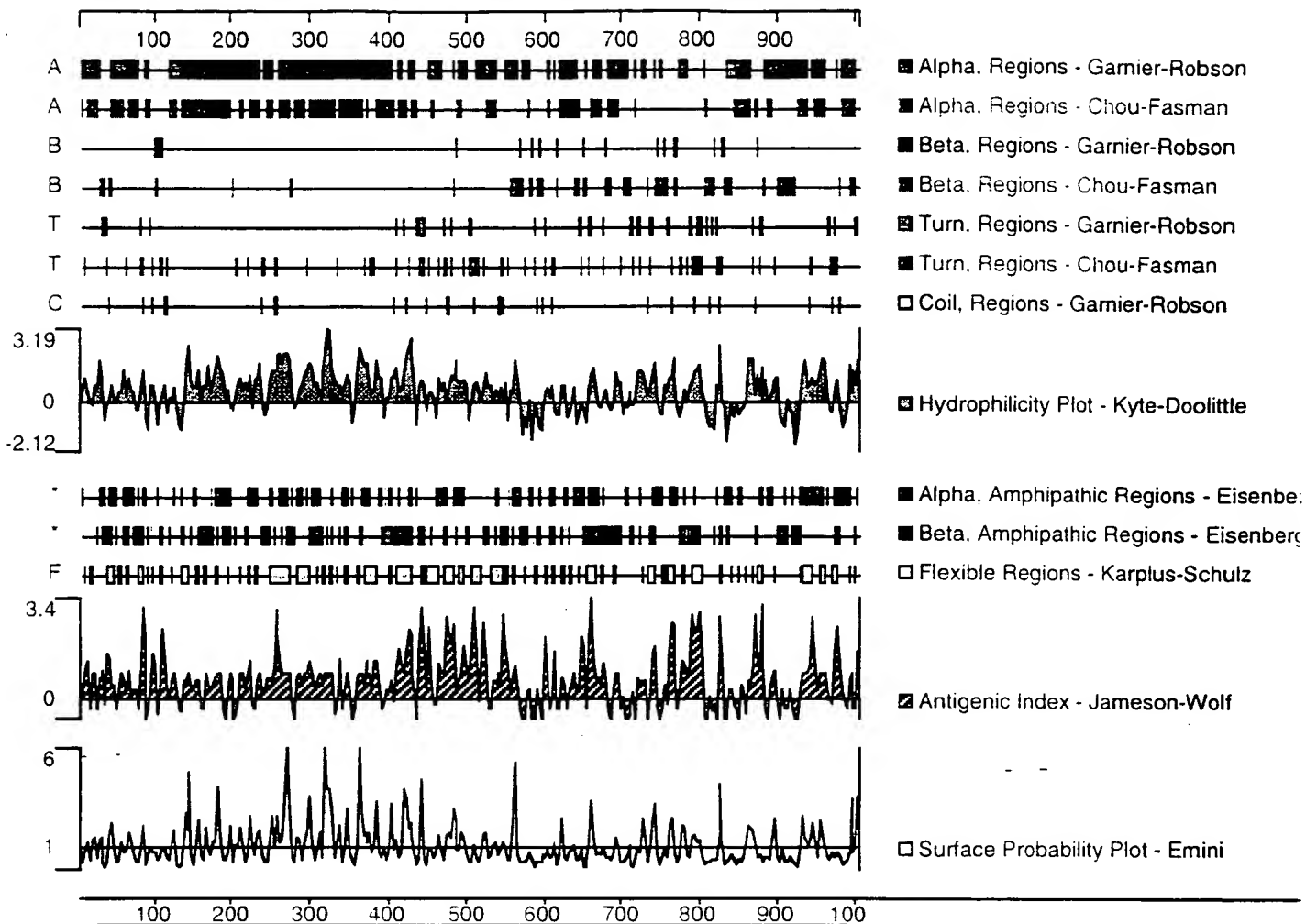


Fig. 4

CARD: domain 1 of 1, from 16 to 107: score -4.1, E = 0.94

\*->aeddrlllrknrllellgeltlsglLdhLleknvLteeeeEkikaknt  
+e + + +r + + +s l +L+++vL + +eE++ +

CARD14 16 EETLWEMMESHRHRIVRCICPSRLTPYLRQAKVLCQLDEEEVLHSPR 62

trr..dkareLiDsvqkkGnqAfqiFlqaLretdqelladlllde<-\*  
+ + +a L+D +++++G + + +Fl++L+ + + + + +

CARD14 63 LTNSAMRAGHLLDLLKTRGKNGAIAFLESCLKFHNPDVYTLVTGLQ 107

Fig. 5A

PDZ domain 1 of 1, from 568 to 659: score 5.3, E = 0.39

PDZ: domain 1 of 1, from 568 to 659: score 5.3, E = 0.39

\*->eitlekevkrnglGfsikggsdk..givvsevlpGsgaAeagGrLke

++t+ ++ 1 +i++ + + +gi++ +v pG +aA++ L++

CARD14 568 QVTMLAF-QGDALLEQISVIGGNltGIFIHRVTPG-SAADQMA-LRP 611

GDvIlsvNG.....qdvenmsheravlaiksgg..evtLtvIRd<-

G +I+ v+ + +++ + +e+ ++e+av +++ g ++++v d

CARD14 612 GTQIVMVDYeaseplfkAVLEDTTLEEAVGLLRVDGfcCLSVKVNTD 659

\*

CARD14

Fig. 5B

SH3\_2: domain 1 of 1, from 679 to 744: score -4.5, E = 3.8

\*->eyvvAlYDyeagnedELsFkkGDiiTvleks..ddgWweGelnr...

+y ++ + e++ +EL ++ +++++v++ ++ g w + + ++ +

CARD14 679 FYIRVNLAMEGRAKGELOVHCNEVLHVTDTMfqGCGCWHHRVNsyt 725

...tGkeGlFPsnYVeeie<-\*

++t G +P + ++

CARD14 726 mkdTAAHGTTIPNYSRAQQQ 744

Fig. 5C





# CARD14-CARD/AD

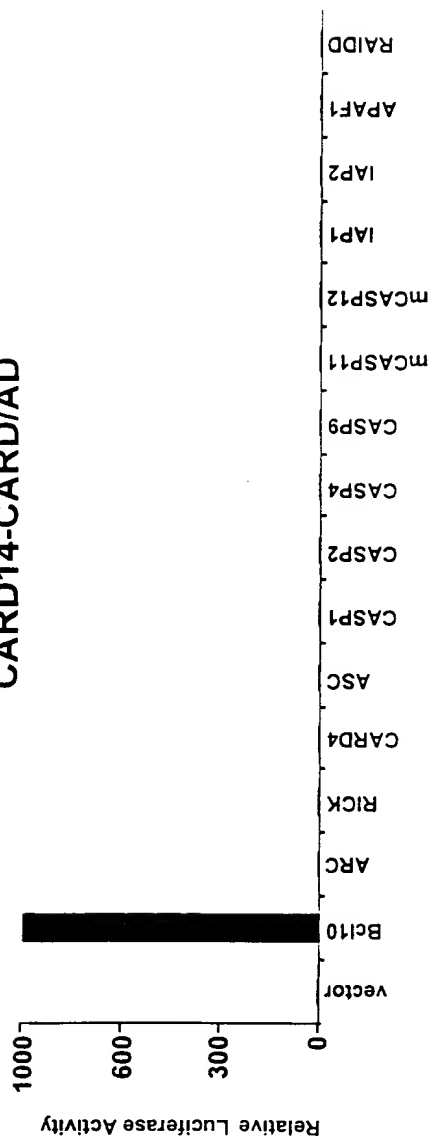


Fig. 6



Western blot analysis showing the levels of Myc-tagged Card11 and Card14 proteins (WB:Myc) and the co-immunoprecipitation of Bcl10 (IP:Bcl10) with these proteins. The blots are shown for six lanes (1-6) corresponding to the experimental conditions detailed in the table below. Molecular weight markers are indicated on the right.

	1	2	3	4	5	6	
WB:Bcl10							== Bcl10
WB:Myc							== Myc-Card11 == Myc-Card14
IP:Bcl10							== Myc-Card11 == Myc-Card14
WB:Myc							== Myc-Card11 == Myc-Card14

	1	2	3	4	5	6	
+	+	-	+	-	-	-	Myc-Card11
-	-	+	-	+	-	-	Myc-Card14
-	-	-	-	-	+	+	control vector



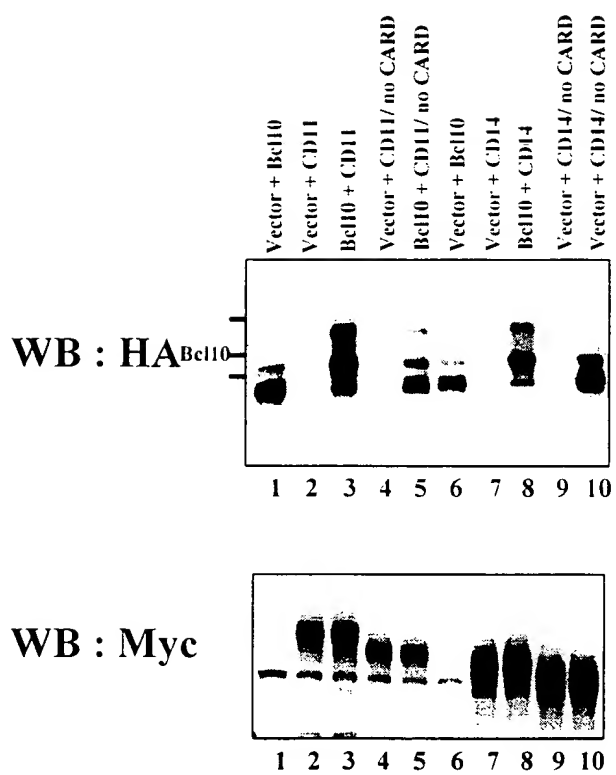


Fig. 8

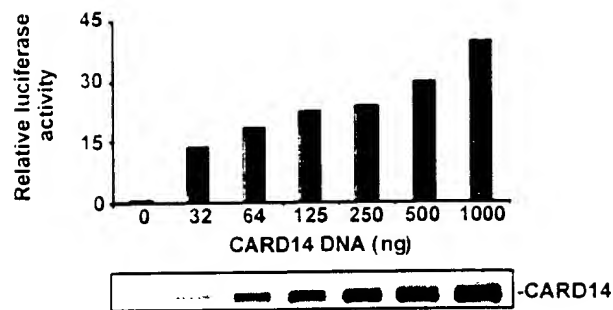


Fig. 9A

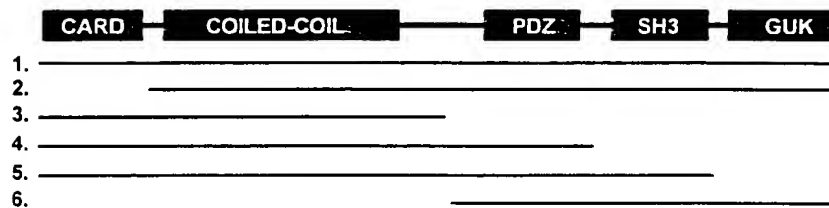


Fig. 9B

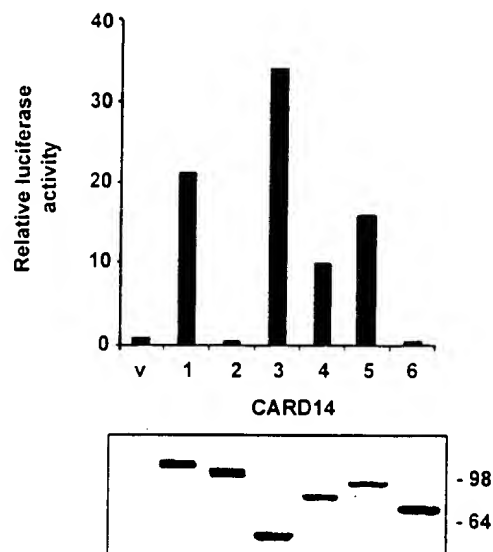


Fig. 9C